

# Chantriolnt-Andreas Kapourani

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## Education

- 2015–Current **PhD in Data Science**, *School of Informatics*, University of Edinburgh.  
*Under the supervision of Prof. Guido Sanguinetti*  
**Thesis:** *Machine learning for computational epigenetics.*  
Develop statistical methods to model (single-cell) epigenetic data and capture spatial correlations of epigenetic marks that would uncover the interplay between genetic and epigenetic mechanisms in transcriptional regulation. Develop probabilistic integrative models for combining multimodal biological data, such as gene expression, DNA methylation and DNA accessibility.
- 2014–2015 **MSc by Research in Data Science**, *School of Informatics*, University of Edinburgh.  
*Distinction*  
**Thesis:** *Mixture modelling of high throughput biomedical data.*  
Mixture modelling of biological data generated from high-throughput sequencing technology. Contributions: 1) Use probabilistic machine learning to extract higher order features associated with the methylation profile across a defined region. 2) Perform Bayesian integrative clustering of heterogeneous types of high-throughput sequencing data generated from different platforms.
- 2012–2013 **MSc in Artificial Intelligence**, *School of Informatics*, University of Edinburgh.  
*Distinction*  
**Thesis:** *Unsupervised motif discovery from acoustic time series data.*  
Discover and extract recurring patterns (i.e. linguistic phrases or words) from input speech data in an unsupervised manner.
- 2008–2012 **Ptychio in Informatics**, *Dept of Informatics and Telematics*, Harokopio University of Athens.  
*Grade 9.1/10 – Distinction*  
**Thesis:** *Integration of external applications in the Unity academic social network environment.*  
Extend the functionality of the Unity academic social network through integration of external applications in the form of Web Services, enabling interoperability with other information systems, using Google's OpenSocial API, a reference for developing social networking environments.
- 2010–2011 **Erasmus Student**, *Department of Computer Science*, Roskilde University, Denmark.  
**Project:** *Find Friend Location*, Distributed real-time location tracking system for Android mobiles provided by SOAP Web Services, <http://rudar.ruc.dk/handle/1800/6198>

## Professional Experience

- 2015–Current **Teaching Assistant**, *School of Informatics*, University of Edinburgh.
- Tutor: Introductory Applied Machine Learning.
  - Demonstrator: Informatics 2B - Algorithms, Data Structures & Learning. Created lab contents: <http://www.inf.ed.ac.uk/teaching/courses/inf2b/learnLabSchedule.html>
  - Marker: Bioinformatics 1 and Informatics 2B - Learning thread.
- 2013–2014 **Junior Developer**, *DaXtra Technologies*.
- DaXtra Technologies is a specialist company in high accuracy, multilingual CV and job parsing as well as semantic search technologies. I was mostly responsible for adapting the company's software to the client needs such as: integration with 3rd party Database Management Systems, integration with web services and online job boards including Indeed, Monster and LinkedIn.

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## Scholarships and Awards

- 2016 Best Paper Award in the 15<sup>th</sup> European Conference on Computational Biology (ECCB).
- 2013 Winner of Travel App Prize (Skyscanner) University of Edinburgh (<http://easyscn.appspot.com/>). Natural Language Processing system for converting natural text to flight queries.
- 2012 Bodossaki Foundation scholarship for postgraduate studies.
- 2009–2012 Scholarship from Greek State Scholarships Foundation (IKY) for excellent performance (Highest Ranked student), for the academic years 2011-2012 (4<sup>th</sup> year), 2010-2011 (3<sup>rd</sup> year), 2009-2010 (2<sup>nd</sup> year), 2008-2009 (1<sup>st</sup> year).

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## Publications

- **Kapourani, C.A.** and Sanguinetti, G. (2018). Melissa: Bayesian clustering and imputation of single cell methylomes. [Preprint] *bioRxiv*, 312025.
- Clark, S.J., Argelaguet, R., **Kapourani, C.A.**, Stubbs, T.M., Lee, H.J., Alda-Catalinas, C., Krueger, F., Sanguinetti, G., Kelsey, G., Marioni, J.C., Stegle, O. and Reik, W., (2018). scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. *Nature communications*, 9(1), p.781.
- **Kapourani, C.A.** and Sanguinetti, G. (2018). BPRMeth: a flexible Bioconductor package for modelling methylation profiles. *Bioinformatics*.
- **Kapourani, C.A.** and Sanguinetti, G. (2016). Higher order methylation features for clustering and prediction in epigenomic studies. *Bioinformatics*, 32 (17), i405-i412. (**Best Paper Award in ECCB 2016**)
- Hatzi, O., Meletakis, G., Katsivelis, P., **Kapourani, C.A.**, Nikolaidou, M. and Anagnostopoulos, D. (2014). Extending the Social Network Interaction Model to Facilitate Collaboration through Service Provision. In *Enterprise, Business-Process and Information Systems Modeling* (pp. 94-108). Springer Berlin Heidelberg.

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## Talks / Tutorials

- Tutorials on machine learning and Bayesian inference: <https://rpubs.com/cakapourani>
- Kapourani, C.A. and Sanguinetti, G., (2018). Bayesian clustering and imputation of single cell methylomes. Oral presentation both on Mathematical and Statistical Aspects of Molecular Biology (MASAMB) workshop 2018 and 13<sup>th</sup> Edinburgh Bioinformatics Meeting. DOI: [10.7490/f1000research.1115317.1](https://doi.org/10.7490/f1000research.1115317.1)
- Kapourani, C.A. and Sanguinetti, G., (2017). Bayesian hierarchical modelling of single-cell methylation profiles. Poster: both on Workshop on Statistical Challenges in Single-Cell Biology, Ascona, Switzerland and ISMB 2017, Prague, Czech Republic.
- Kapourani, C.A. and Sanguinetti, G., (2016). Higher order methylation features for clustering and prediction in epigenomic studies. 15<sup>th</sup> European Conference on Computational Biology (ECCB). The Hague, Netherlands. DOI: [10.7490/f1000research.1113102.1](https://doi.org/10.7490/f1000research.1113102.1)
- Kapourani, C.A. and Sanguinetti, G., (2016). Bayesian integrative clustering of heterogeneous types of high-throughput sequencing data. 10<sup>th</sup> *International Workshop on Machine Learning in Systems Biology (MLSB)*. The Hague, Netherlands.
- Kapourani, C.A. and Sanguinetti, G., (2015). Mixture Modelling of DNA Methylation Profiles. *Workshop in Statistical Modeling of Epigenomics and Gene Regulation (SMEGR)*. Harvard University, USA.

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## Skills

- ML / Stats Generalized Linear Models, Bayesian inference, Variational Inference, Gaussian Processes, Approximate inference, Optimization, Latent Variable Models, Graphical Models, Mixture models, Neural Networks, Markov Chain Monte Carlo, Kernel methods, Hidden Markov Models.
- Languages R, Python, Java, C/C++, MATLAB, PHP, SQL, HTML, JavaScript, BPMN, PROLOG, L<sup>A</sup>T<sub>E</sub>X.
- Technologies Hadoop/MapReduce, Android Development, AJAX, JSP, Git, Web Services (SOAP, REST).
- Databases MySQL, Oracle.
- IDEs RStudio, Eclipse, NetBeans, Spyder, JDeveloper.